

- 1 -

```
<110> Asundi, Vinod
      Ford, John E.
      Drmanac, Radoje T.
      Liu, Chenghua
      Tang, Y. Tom
      Yamasaki, Vicky
      Yeung, George
      Zhang, Jie
      Zhou, Ping
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&lt;120&gt; EGF MOTIF PROTEIN, EGFL6, MATERIALS AND METHODS

<130> 28110/36737

<150> US 09/620,312

<151> 2000-07-19

<150> US 09/363,316

<151> 1999-07-28

&lt;160&gt; 32

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

$\langle 222 \rangle \quad (1) \dots (300)$

<221> misc feature

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<223> n = A, T, C or G

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gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt 96  
Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe  
20 25 30

cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga 144  
Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly  
35 40 45

atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc 192  
Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser  
50 55 60

tac	aag	tgc	ttt	tgc	ctc	agt	ggc	cac	atg	ctc	atg	cca	gat	gct	acg	240
Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	
65					70					75					80	

tgt	gtg	aac	tcn	agg	aca	tgt	gcc	atg	ata	aac	tgt	cag	tat	agc	tgt	288
Cys	Val	Asn	Xaa	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	
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<221> misc_feature
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																432
																480
																528

cat acg tgc agc cac cat gcc aat tgc ttc aat acc caa ggg tcc ttc	576
His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe	
180 185 190	
aag tgt aaa tgc aag cag gga tat aaa ggc aat gga ctt cgg tgt tct	624
Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser	
195 200 205	
gct atc cct gaa aat tct gtg aag gaa gtc ctc aga gca cct ggt acc	672
Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr	
210 215 220	
atc aaa gac aga atc aag aag ttg ctt gct cac aaa aac agc atg aaa	720
Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys	
225 230 235 240	
aag aag gca aaa att aaa aat gtt acc cca gaa ccc acc agg act cct	768
Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro	
245 250 255	
acc cct aag gtg aac ttg cag ccc ttc aac tat gaa gag ata gtt tcc	816
Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser	
260 265 270	
aga ggc ggg aac tct cat gga ggt aaa aaa ggg aat gaa gag aaa atg	864
Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met	
275 280 285	
aaa gag ggg ctt gag gat gag aaa aga gaa gag aaa gcc ctg aag aat	912
Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn	
290 295 300	
gac ata gag gag cga agc ctg cga gga gat gtg ttt ttc cct aag gtg	960
Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val	
305 310 315 320	
aat gaa gca ggt gaa ttc ggc ctg att ctg gtc caa agg aaa gcg cta	1008
Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu	
325 330 335	
act tcc aaa ctg gaa cat aaa gat tta aat atc tcg gtt gac tgc agc	1056
Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser	
340 345 350	
ttc aat cat ggg atc tgt gac tgg aaa cag gat aga gaa gat gat ttt	1104
Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe	
355 360 365	
gac tgg aat cct gct gat cga gat aat gct att ggc ttc tat atg gca	1152
Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala	
370 375 380	
gtt ccg gcc ttg gca ggt cac atg aaa gac att ggc cga ttg aaa ctt	1200
Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu	
385 390 395 400	
ctc cta cct gac ctg caa ccc caa agc aac ttc tgt ttg ctc ttt gat	1248
Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp	
405 410 415	
tac cgg ctg gcc gga gac aaa gtc ggg aaa ctt cga gtg ttt gtg aaa	1296
Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys	
420 425 430	

00607860 101300

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Pro	Gly	Tyr 35	Thr	Gly	Lys	Thr	Cys 40	Ser	Gln	Asp	Val	Asn 45	Glu	Cys	Gly
Met	Lys 50	Pro	Arg	Pro	Cys	Gln 55	His	Arg	Cys	Val	Asn 60	Thr	His	Gly	Ser

Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr
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Cys	Val	Asn	Ser	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys
				85					90					95	
Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu
			100					105					110		
Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala
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Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe
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Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile
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Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	Asp	Ser
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His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	Gly	Ser	Phe
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Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	Leu	Arg	Cys	Ser
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Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	Arg	Ala	Pro	Gly	Thr
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Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	His	Lys	Asn	Ser	Met	Lys
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Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	Pro	Glu	Pro	Thr	Arg	Thr	Pro
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Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	Phe	Asn	Tyr	Glu	Glu	Ile	Val	Ser
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Lys	Glu	Gly	Leu	Glu	Asp	Glu	Lys	Arg	Glu	Glu	Lys	Ala	Leu	Lys	Asn
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Asp	Ile	Glu	Glu	Arg	Ser	Leu	Arg	Gly	Asp	Val	Phe	Phe	Pro	Lys	Val
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Asn	Glu	Ala	Gly	Glu	Phe	Gly	Leu	Ile	Leu	Val	Gln	Arg	Lys	Ala	Leu
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Thr	Ser	Lys	Leu	Glu	His	Lys	Asp	Leu	Asn	Ile	Ser	Val	Asp	Cys	Ser
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Phe	Asn	His	Gly	Ile	Cys	Asp	Trp	Lys	Gln	Asp	Arg	Glu	Asp	Asp	Phe
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Asp	Trp	Asn	Pro	Ala	Asp	Arg	Asp	Asn	Ala	Ile	Gly	Phe	Tyr	Met	Ala
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Val	Pro	Ala	Leu	Ala	Gly	His	Met	Lys	Asp	Ile	Gly	Arg	Leu	Lys	Leu
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Leu	Leu	Pro	Asp	Leu	Gln	Pro	Gln	Ser	Asn	Phe	Cys	Leu	Leu	Phe	Asp
			405						410					415	
Tyr	Arg	Leu	Ala	Gly	Asp	Lys	Val	Gly	Lys	Leu	Arg	Val	Phe	Val	Lys
			420					425					430		
Asn	Ser	Asn	Asn	Ala	Leu	Ala	Trp	Glu	Lys	Thr	Thr	Ser	Glu	Asp	Glu
		435					440					445			
Lys	Trp	Lys	Thr	Gly	Lys	Ile	Gln	Leu	Tyr	Gln	Gly	Thr	Asp	Ala	Thr
	450					455					460				
Lys	Ser	Ile	Ile	Phe	Glu	Ala	Glu	Arg	Gly	Lys	Gly	Lys	Thr	Gly	Glu
465					470					475					480
Ile	Ala	Val	Asp	Gly	Val	Leu	Leu	Val	Ser	Gly	Leu	Cys	Pro	Asp	Ser
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Leu	Leu	Ser	Val	Asp	Asp	Xaa	Met	Val	Leu	Ser	Leu	Tyr	Leu	Thr	Leu
			500					505					510		
Tyr	Val	Ser	Ser	Leu	Val	Phe	Leu	Ile	Leu	His	His	Arg	Thr	Ser	Gly
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Ile Leu Lys Leu Leu Ala Glu Lys Leu  
530 535

00607850-101300



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Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys	
205 210 215	
ata gat ata aat gaa tgt act atg gat agc cat acg tgc agc cac cat	903
Ile Asp Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His	
220 225 230	
gcc aat tgc ttc aat acc caa ggg tcc ttc aag tgt aaa tgc aag cag	951
Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln	
235 240 245	
gga tat aaa ggc aat gga ctt cgg tgt tct gct atc cct gaa aat tct	999
Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser	
250 255 260 265	
gtg aag gaa gtc ctc aga gca cct ggt acc atc aaa gac aga atc aag	1047
Val Lys Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys	
270 275 280	
aag ttg ctt gct cac aaa aac agc atg aaa aag aag gca aaa att aaa	1095
Lys Leu Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys	
285 290 295	
aat gtt acc cca gaa ccc acc agg act cct acc cct aag gtg aac ttg	1143
Asn Val Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu	
300 305 310	
cag ccc ttc aac tat gaa gag ata gtt tcc aga ggc ggg aac tct cat	1191
Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His	
315 320 325	
gga ggt aaa aaa ggg aat gaa gag aaa atg aaa gag ggg ctt gag gat	1239
Gly Gly Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp	
330 335 340 345	
gag aaa aga gaa gag aaa gcc ctg aag aat gac wta gag gag cga agc	1287
Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn Asp Xaa Glu Glu Arg Ser	
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Leu Arg Gly Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly Glu Phe	
365 370 375	
ggc ctg att ctg gtc caa agg aaa gcg cta act tcc aaa ctg gaa cat	1383
Gly Leu Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His	
380 385 390	
aaa gat tta aat atc tcg gtt gac tgc agc ttc aat cat ggg atc tgt	1431
Lys Asp Leu Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys	
395 400 405	
gac tgg aaa cag gat aga gaa gat gat ttt gac tgg aat cct gct gat	1479
Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp	
410 415 420 425	
cga gat aat gct att ggc ttc tat atg gca gtt ccg gcc ttg gca ggt	1527
Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly	
430 435 440	
cac aag aaa gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa	1575
His Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln	
445 450 455	

00607860 101300

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ccc caa agc aac ttc tgt ttg ctc ttt gat tac cgg ctg gcc gga gac      1623
Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp
      460                      465                      470

aaa gtc ggg aaa ctt cga gtg ttt gtg aaa aac agt aac aat gcc ctg      1671
Lys Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu
      475                      480                      485

gca tgg gag aag acc acg agt gag gat gaa aag tgg aag aca ggg aaa      1719
Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys
      490                      495                      500                      505

att cag ttg tat caa gga act gat gct acc aaa agc atc att ttt gaa      1767
Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu
      510                      515                      520

gca gaa cgt ggc aag ggc aaa acc ggc gaa atc gca gtg gat ggc gtc      1815
Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp Gly Val
      525                      530                      535

ttg ctt gtt tca ggc tta tgt cca gat agc ctt tta tct gtg gat gac      1863
Leu Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val Asp Asp
      540                      545                      550

tga atgttactat ctttatatatt gactttgtat gtcagttccc tggttttttt      1916
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gatattgsat cataggacct ctggcatttt aaaattacta agctgaaaaa ttgtaatgta      1976
ccaacagaaa ttattattgt aagatgcctt tmttgataaa gatatgcaa tatttgcttt      2036
aaatatcata tcaactgtatc ttctcagtc tttctgaatc tttccacatt atattataaa      2096
atatggaaat gtcagggttta tctccctcc tcaagtatac tgatttgtat aagtaagttg      2156
atgagcttct ctctgcaaca tttctagaaa atagahaaaa aagcacagag aaatgtttta      2216
ctgtttgact cttatgatag tttttggaaa ctatgacatc aaagatagac ttttgccata      2276
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<210> 6
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<212> PRT
<213> Homo sapiens

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      20          25          30
Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly Thr Lys Leu Ala
      35          40          45
Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr
      50          55          60
Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys
      65          70          75          80
Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn
      85          90          95
Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr
      100          105          110
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00607860.101300



His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro
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	130					135				140					
Tyr	Ser	Cys	Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser
145				150						155					160
Ser	Gly	Leu	Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp
			165						170					175	
Glu	Cys	Ala	Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val
		180						185				190			
Asn	Thr	Phe	Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu
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Gln	Tyr	Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr
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Met	Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln
225					230					235					240
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	Leu
			245						250					255	
Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	Arg	Ala
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Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	His	Lys	Asn
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Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	Pro	Glu	Pro	Thr
	290					295					300				
Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	Phe	Asn	Tyr	Glu	Glu
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Ile	Val	Ser	Arg	Gly	Gly	Asn	Ser	His	Gly	Gly	Lys	Lys	Gly	Asn	Glu
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Glu	Lys	Met	Lys	Glu	Gly	Leu	Glu	Asp	Glu	Lys	Arg	Glu	Glu	Lys	Ala
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Leu	Lys	Asn	Asp	Xaa	Glu	Glu	Arg	Ser	Leu	Arg	Gly	Asp	Val	Phe	Phe
		355					360					365			
Pro	Lys	Val	Asn	Glu	Ala	Gly	Glu	Phe	Gly	Leu	Ile	Leu	Val	Gln	Arg
	370					375					380				
Lys	Ala	Leu	Thr	Ser	Lys	Leu	Glu	His	Lys	Asp	Leu	Asn	Ile	Ser	Val
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Asp	Cys	Ser	Phe	Asn	His	Gly	Ile	Cys	Asp	Trp	Lys	Gln	Asp	Arg	Glu
			405						410					415	
Asp	Asp	Phe	Asp	Trp	Asn	Pro	Ala	Asp	Arg	Asp	Asn	Ala	Ile	Gly	Phe
			420					425					430		
Tyr	Met	Ala	Val	Pro	Ala	Leu	Ala	Gly	His	Lys	Lys	Asp	Ile	Gly	Arg
		435					440					445			
Leu	Lys	Leu	Leu	Leu	Pro	Asp	Leu	Gln	Pro	Gln	Ser	Asn	Phe	Cys	Leu
	450					455					460				
Leu	Phe	Asp	Tyr	Arg	Leu	Ala	Gly	Asp	Lys	Val	Gly	Lys	Leu	Arg	Val
465					470					475					480
Phe	Val	Lys	Asn	Ser	Asn	Asn	Ala	Leu	Ala	Trp	Glu	Lys	Thr	Thr	Ser
			485						490					495	
Glu	Asp	Glu	Lys	Trp	Lys	Thr	Gly	Lys	Ile	Gln	Leu	Tyr	Gln	Gly	Thr
		500						505					510		
Asp	Ala	Thr	Lys	Ser	Ile	Ile	Phe	Glu	Ala	Glu	Arg	Gly	Lys	Gly	Lys
	515						520					525			
Thr	Gly	Glu	Ile	Ala	Val	Asp	Gly	Val	Leu	Leu	Val	Ser	Gly	Leu	Cys
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Pro	Asp	Ser	Leu	Leu	Ser	Val	Asp	Asp							
545					550										

<210> 7  
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 <212> PRT  
 <213> Drosophila Melanogaster

00687860-101300

<220>  
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 <223> Xaa = Any Amino Acid

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 Thr Gly Lys Xaa Xaa Xaa Cys Glu Xaa Asn  
 35 40

<210> 8  
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 <212> PRT  
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<220>  
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 20 25 30  
 Gly Xaa Xaa Leu Xaa Cys Asp  
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<210> 9  
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 <212> PRT  
 <213> Homo sapiens

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 20 25 30  
 His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro  
 35 40 45  
 Asp Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys  
 50 55 60  
 Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu  
 65 70 75 80  
 Arg Leu Ala Pro Asn Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys  
 85 90 95  
 Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys  
 100 105 110  
 Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Ile Asn Glu  
 115 120 125  
 Cys Thr Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn  
 130 135 140  
 Thr Gln Gly Ser Phe Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly  
 145 150 155 160  
 Leu Arg Cys Ser

<210> 10  
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 <212> PRT

00ET07"09028960

<223> Xaa = Any Amino Acid

Val	Xaa	Glu	Cys	Xaa	Ser	Gly	Xaa	Gln	Xaa	Xaa	Cys	Xaa	Ser	Ser	Xaa
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Xaa	Cys	Xaa	Asn	Thr	Val	Gly	Ser	Tyr	Xaa	Cys	Arg	Cys	Arg	Pro	Gly
			20					25					30		
Trp	Xaa	Pro	Xaa	Pro	Gly	Xaa	Pro	Asn	Xaa	Xaa	Xaa	Asp			
		35					40					45			

<213> Mammalian

<223> Xaa = Any Amino Acid

Asn	Ser	Asp	Ser	Glu	Cys	Pro	Leu	Ser	His	Asp	Gly	Tyr	Cys	Leu	His
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Asp	Gly	Val	Cys	Met	Tyr	Ile	Glu	Ala	Leu	Asp	Lys	Tyr	Ala	Cys	Asn
			20					25					30		
Cys	Val	Val	Gly	Tyr	Ile	Xaa	Xaa	Xaa	Gly	Glu	Arg	Xaa	Xaa	Cys	Gln
		35					40					45			
Tyr	Arg	Asp	Leu	Lys	Trp	Trp	Glu	Leu	Arg						
	50					55									

<213> Artificial Sequence

<223> Gene-specific PCR primer 10244-52

21

<213> Artificial Sequence

<223> Gene-specific PCR primer 10244-51

21

<213> Artificial Sequence

<220>

<400> 14

21

<210> 15

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Vector primer SP6

<400> 15

22

<210> 16

$\langle 211 \rangle$  21

<212> DNA

<213> Artificial Sequence

<220>

<223> Gene-specific PCR primer 10244-A

<400> 16

21

<210> 17

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Gene-specific PCR primer 10244-B

<400> 17

21

<210> 18

<211> 502

<212> PRT

<213> Homo sapiens

<220>

## <221> VARIANT

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<223> Xaa = Any Amino Acid

<400> 18

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Gly	Cys	Lys	Phe 20	Gly	Glu	Cys	Val	Gly 25	Pro	Asn	Lys	Cys	Arg 30	Cys	Phe
Pro	Gly	Tyr 35	Thr	Gly	Lys	Thr	Cys 40	Ser	Gln	Asp	Val	Asn 45	Glu	Cys	Gly
Met	Lys 50	Pro	Arg	Pro	Cys	Gln 55	His	Arg	Cys	Val	Asn 60	Thr	His	Gly	Ser
Tyr 65	Lys	Cys	Phe	Cys	Leu 70	Ser	Gly	His	Met	Leu 75	Met	Pro	Asp	Ala	Thr 80
Cys	Val	Asn	Ser	Arg 85	Thr	Cys	Ala	Met	Ile 90	Asn	Cys	Gln	Tyr	Ser 95	Cys
Glu	Asp	Thr	Glu 100	Gly	Pro	Gln	Cys 105	Leu	Cys	Pro	Ser	Ser 110	Gly	Leu	



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<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 21
ccagaaccca ccaggactcc                                       20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 22
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<210> 23
<211> 2365
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (205) .. (1863)

<400> 23
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ggagggcggcg gcttagctgc tacgggggtcc ggccggcgcc ctcccgaggg gggctcagga 180
ggaggaagga ggacccgtgc gaga atg cct ctg ccc tgg agc ctt gcg ctc      231
                        Met Pro Leu Pro Trp Ser Leu Ala Leu
                        1                      5

ccg ctg ctg ctc tcc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt      279
Pro Leu Leu Leu Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser
10                      15                      20                      25

gca agg cat cac ggg ttg tta gca tcg gca cgt cag cct ggg gtc tgt      327
Ala Arg His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys
                        30                      35                      40

cac tat gga act aaa ctg gcc tgc tgc tac ggc tgg aga aga aac agc      375
His Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser
                        45                      50                      55

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00ET07"09828950

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Lys	Gly	Val	Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	
		60						65					70			
tgc	gtg	gga	cca	aac	aaa	tgc	aga	tgc	ttt	cca	gga	tac	acc	ggg	aaa	471
Cys	Val	Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	
	75					80					85					
acc	tgc	agt	caa	gat	gtg	aat	gag	tgt	gga	atg	aaa	ccc	cgg	cca	tgc	519
Thr	Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	
	90				95					100					105	
caa	cac	aga	tgt	gtg	aat	aca	cac	gga	agc	tac	aag	tgc	ttt	tgc	ctc	567
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	Leu	
				110					115					120		
agt	ggc	cac	atg	ctc	atg	cca	gat	gct	acg	tgt	gtg	aac	tct	agg	aca	615
Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	Arg	Thr	
			125					130					135			
tgt	gcc	atg	ata	aac	tgt	cag	tat	agc	tgt	gaa	gac	aca	gaa	gaa	ggg	663
Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	Glu	Glu	Gly	
		140					145					150				
cca	cag	tgc	ctg	tgt	cca	tcc	tca	gga	ctc	cgc	ctg	gcc	cca	aat	gga	711
Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	Ala	Pro	Asn	Gly	
	155					160					165					
aga	gac	tgt	cta	gat	att	gat	gaa	tgt	gcc	tct	ggg	aaa	gtc	atc	tgt	759
Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	Gly	Lys	Val	Ile	Cys	
	170				175					180					185	
ccc	tac	aat	cga	aga	tgt	gtg	aac	aca	ttt	gga	agc	tac	tac	tgc	aaa	807
Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	Gly	Ser	Tyr	Tyr	Cys	Lys	
				190					195					200		
tgt	cac	att	ggg	ttc	gaa	ctg	caa	tat	atc	agt	gga	cga	tat	gac	tgt	855
Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile	Ser	Gly	Arg	Tyr	Asp	Cys	
			205					210					215			
ata	gat	ata	aat	gaa	tgt	act	atg	gat	agc	cat	acg	tgc	agc	cac	cat	903
Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	Asp	Ser	His	Thr	Cys	Ser	His	His	
		220					225					230				
gcc	aat	tgc	ttc	aat	acc	caa	ggg	tcc	ttc	aag	tgt	aaa	tgc	aag	cag	951
Ala	Asn	Cys	Phe	Asn	Thr	Gln	Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	
	235					240					245					
gga	tat	aaa	ggc	aat	gga	ctt	cgg	tgt	tct	gct	atc	cct	gaa	aat	tct	999
Gly	Tyr	Lys	Gly	Asn	Gly	Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	
	250				255					260					265	
gtg	aag	gaa	gtc	ctc	aga	gca	cct	ggg	acc	atc	aaa	gac	aga	atc	aag	1047
Val	Lys	Glu	Val	Leu	Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	
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aag	ttg	ctt	gct	cac	aaa	aac	agc	atg	aaa	aag	aag	gca	aaa	att	aaa	1095
Lys	Leu	Leu	Ala	His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	
			285					290					295			
aat	gtt	acc	cca	gaa	ccc	acc	agg	act	cct	acc	cct	aag	gtg	aac	ttg	1143
Asn	Val	Thr	Pro	Glu	Pro	Thr	Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	
		300					305					310				

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cag	ccc	ttc	aac	tat	gaa	gag	ata	gtt	tcc	aga	ggc	ggg	aac	tct	cat	1191
Gln	Pro	Phe	Asn	Tyr	Glu	Glu	Ile	Val	Ser	Arg	Gly	Gly	Asn	Ser	His	
	315					320					325					
gga	ggt	aaa	aaa	ggg	aat	gaa	gag	aaa	atg	aaa	gag	ggg	ctt	gag	gat	1239
Gly	Gly	Lys	Lys	Gly	Asn	Glu	Glu	Lys	Met	Lys	Glu	Gly	Leu	Glu	Asp	
330					335					340					345	
gag	aaa	aga	gaa	gag	aaa	gcc	ctg	aag	aat	gac	ata	gag	gag	cga	agc	1287
Glu	Lys	Arg	Glu	Glu	Lys	Ala	Leu	Lys	Asn	Asp	Ile	Glu	Glu	Arg	Ser	
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ctg	cga	gga	gat	gtg	ttt	ttc	cct	aag	gtg	aat	gaa	gca	ggg	gaa	ttc	1335
Leu	Arg	Gly	Asp	Val	Phe	Phe	Pro	Lys	Val	Asn	Glu	Ala	Gly	Glu	Phe	
			365					370					375			
ggc	ctg	att	ctg	gtc	caa	agg	aaa	gcg	cta	act	tcc	aaa	ctg	gaa	cat	1383
Gly	Leu	Ile	Leu	Val	Gln	Arg	Lys	Ala	Leu	Thr	Ser	Lys	Leu	Glu	His	
		380					385					390				
aaa	gat	tta	aat	atc	tcg	gtt	gac	tgc	agc	ttc	aat	cat	ggg	atc	tgt	1431
Lys	Asp	Leu	Asn	Ile	Ser	Val	Asp	Cys	Ser	Phe	Asn	His	Gly	Ile	Cys	
	395					400					405					
gac	tgg	aaa	cag	gat	aga	gaa	gat	gat	ttt	gac	tgg	aat	cct	gct	gat	1479
Asp	Trp	Lys	Gln	Asp	Arg	Glu	Asp	Asp	Phe	Asp	Trp	Asn	Pro	Ala	Asp	
410					415					420					425	
cga	gat	aat	gct	att	ggc	ttc	tat	atg	gca	gtt	ccg	gcc	ttg	gca	ggg	1527
Arg	Asp	Asn	Ala	Ile	Gly	Phe	Tyr	Met	Ala	Val	Pro	Ala	Leu	Ala	Gly	
				430					435					440		
cac	aag	aaa	gac	att	ggc	cga	ttg	aaa	ctt	ctc	cta	cct	gac	ctg	caa	1575
His	Lys	Lys	Asp	Ile	Gly	Arg	Leu	Lys	Leu	Leu	Leu	Pro	Asp	Leu	Gln	
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ccc	caa	agc	aac	ttc	tgt	ttg	ctc	ttt	gat	tac	cgg	ctg	gcc	gga	gac	1623
Pro	Gln	Ser	Asn	Phe	Cys	Leu	Leu	Phe	Asp	Tyr	Arg	Leu	Ala	Gly	Asp	
		460					465					470				
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Lys	Val	Gly	Lys	Leu	Arg	Val	Phe	Val	Lys	Asn	Ser	Asn	Asn	Ala	Leu	
	475					480					485					
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Ala	Trp	Glu	Lys	Thr	Thr	Ser	Glu	Asp	Glu	Lys	Trp	Lys	Thr	Gly	Lys	
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att	cag	ttg	tat	caa	gga	act	gat	gct	acc	aaa	agc	atc	att	ttt	gaa	1767
Ile	Gln	Leu	Tyr	Gln	Gly	Thr	Asp	Ala	Thr	Lys	Ser	Ile	Ile	Phe	Glu	
				510					515					520		
gca	gaa	cgt	ggc	aag	ggc	aaa	acc	ggc	gaa	atc	gca	gtg	gat	ggc	gtc	1815
Ala	Glu	Arg	Gly	Lys	Gly	Lys	Thr	Gly	Glu	Ile	Ala	Val	Asp	Gly	Val	
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ttg	ctt	gtt	tca	ggc	tta	tgt	cca	gat	agc	ctt	tta	tct	gtg	gat	gac	1863
Leu	Leu	Val	Ser	Gly	Leu	Cys	Pro	Asp	Ser	Leu	Leu	Ser	Val	Asp	Asp	
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satcatagga	cctctggcat	tttaaaatta	ctaagctgaa	aaattgtaat	gtaccaacag	1983										



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<210> 24  
 <211> 553  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> VARIANT  
 <222> (1)...(553)

<400> 24

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			20					25					30		
Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	Lys	Leu	Ala
		35					40					45			
Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	Cys	Glu	Ala	Thr
	50					55					60				
Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	Gly	Pro	Asn	Lys	Cys
	65				70					75					80
Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser	Gln	Asp	Val	Asn
				85					90					95	
Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg	Cys	Val	Asn	Thr
			100					105					110		
His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro
		115					120					125			
Asp	Ala	Thr	Cys	Val	Asn	Ser	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln
	130						135				140				
Tyr	Ser	Cys	Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser
145				150						155				160	
Ser	Gly	Leu	Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp
			165					170					175		
Glu	Cys	Ala	Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val
			180					185					190		

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Pro Asp Ser Leu Leu Ser Val Asp Asp  
545 550

<220>  
<223> Description of Artificial Sequence: Primer

```
<210> 26
<211> 30
<212> DNA
<213> Artificial Sequence
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<210> 27
<211> 2360
<212> DNA
<213> Homo sapiens
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<220>  
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<222> (1)...(2360)  
<223> n = a,t,c or g
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<400> 27
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ctgctacggg gtccggggccg gcgccctccc gagggggggct caggaggagg aaggaggacc      180
cgtgcgaga      atg cct ctg ccc tgg agc ctt gcg ctc ccg ctg ctg ctc      228
                Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Leu
                1                5                10

tcc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt gca agg ggt tct      276
Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg Gly Ser
 14                19                24                29

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cat	cat	cat	cat	cat	cac	ggg	ttg	tta	gca	tcg	gca	cgt	cag	cct	ggg	324
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Val	Cys	His	Tyr	Gly	Thr	Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	
46					51					56					61	
aac	agc	aag	gga	gtc	tgt	gaa	gct	aca	tgc	gaa	cct	gga	tgt	aag	ttt	420
Asn	Ser	Lys	Gly	Val	Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	
62					67					72					77	
ggg	gag	tgc	gtg	gga	cca	aac	aaa	tgc	aga	tgc	ttt	cca	gga	tac	acc	468
Gly	Glu	Cys	Val	Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	
78					83					88					93	
ggg	aaa	acc	tgc	agt	caa	gat	gtg	aat	gag	tgt	gga	atg	aaa	ccc	cgg	516
Gly	Lys	Thr	Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	
94					99					104					109	
cca	tgc	caa	cac	aga	tgt	gtg	aat	aca	cac	gga	agc	tac	aag	tgc	ttt	564
Pro	Cys	Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	
110					115					120					125	
tgc	ctc	agt	ggc	cac	atg	ctc	atg	cca	gat	gct	acg	tgt	gtg	aac	tct	612
Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	
126					131					136					141	
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Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	Glu	
142					147					152					157	
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Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	Ala	Pro	
158					163					168					173	
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Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	Gly	Lys	Val	
174					179					184					189	
atc	tgt	ccc	tac	aat	cga	aga	tgt	gtg	aac	aca	ttt	gga	agc	tac	tac	804
Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	Gly	Ser	Tyr	Tyr	
190					195					200					205	
tgc	aaa	tgt	cac	att	ggg	ttc	gaa	ctg	caa	tat	atc	agt	gga	cga	tat	852
Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile	Ser	Gly	Arg	Tyr	
206					211					216					221	
gac	tgt	ata	gat	ata	aat	gaa	tgt	act	atg	gat	agc	cat	acg	tgc	agc	900
Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	Asp	Ser	His	Thr	Cys	Ser	
222					227					232					237	
cac	cat	gcc	aat	tgc	ttc	aat	acc	caa	ggg	tcc	ttc	aag	tgt	aaa	tgc	948
His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	Gly	Ser	Phe	Lys	Cys	Lys	Cys	
238					243					248					253	
aag	cag	gga	tat	aaa	ggc	aat	gga	ctt	cgg	tgt	tct	gct	atc	cct	gaa	996
Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	
254					259					264					269	
aat	tct	gtg	aag	gaa	gtc	ctc	aga	gca	cct	ggg	acc	atc	aaa	gac	aga	1044
Asn	Ser	Val	Lys	Glu	Val	Leu	Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	
270					275					280					285	

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aac Asn 318	ttg Leu	cag Gln	ccc Pro	ttc Phe	aac Asn 323	tat Tyr	gaa Glu	gag Glu	ata Ile	gtt Val 328	tcc Ser	aga Arg	ggc Gly	ggg Gly	aac Asn 333	1188
tct Ser 334	cat His	gga Gly	ggg Gly	aaa Lys	aaa Lys 339	ggg Gly	aat Asn	gaa Glu	gag Glu	aaa Lys 344	atg Met	aaa Lys	gag Glu	ggg Gly	ctt Leu 349	1236
gag Glu 350	gat Asp	gag Glu	aaa Lys	aga Arg	gaa Glu 355	gag Glu	aaa Lys	gcc Ala	ctg Leu	aag Lys 360	aat Asn	gac Asp	ata Ile	gag Glu	gag Glu 365	1284
cga Arg 366	agc Ser	ctg Leu	cga Arg	gga Gly	gat Asp 371	gtg Val	ttt Phe	ttc Phe	cct Pro	aag Lys 376	gtg Val	aat Asn	gaa Glu	gca Ala	ggg Gly 381	1332
gaa Glu 382	ttc Phe	ggc Gly	ctg Leu	att Ile	ctg Leu 387	gtc Val	caa Gln	agg Arg	aaa Lys	gcg Ala 392	cta Leu	act Thr	tcc Ser	aaa Lys	ctg Leu 397	1380
gaa Glu 398	cat His	aaa Lys	gat Asp	tta Leu	aat Asn 403	atc Ile	tgc Ser	gtt Val	gac Asp	tgc Cys 408	agc Ser	ttc Phe	aat Asn	cat His	ggg Gly 413	1428
atc Ile 414	tgt Cys	gac Asp	tgg Trp	aaa Lys	cag Gln 419	gat Asp	aga Arg	gaa Glu	gat Asp	gat Asp 424	ttt Phe	gac Asp	tgg Trp	aat Asn	cct Pro 429	1476
gct Ala 430	gat Asp	cga Arg	gat Asp	aat Asn	gct Ala 435	att Ile	ggc Gly	ttc Phe	tat Tyr	atg Met 440	gca Ala	gtt Val	ccg Pro	gcc Ala	ttg Leu 445	1524
gca Ala 446	ggg Gly	cac His	aag Lys	aaa Lys	gac Asp 451	att Ile	ggc Gly	cga Arg	ttg Leu	aaa Lys 456	ctt Leu	ctc Leu	cta Leu	cct Pro	gac Asp 461	1572
ctg Leu 462	caa Gln	ccc Pro	caa Gln	agc Ser	aac Asn 467	ttc Phe	tgt Cys	ttg Leu	ctc Leu	ttt Phe 472	gat Asp	tac Tyr	cgg Arg	ctg Leu	gcc Ala 477	1620
gga Gly 478	gac Asp	aaa Lys	gtc Val	ggg Gly	aaa Lys 483	ctt Leu	cga Arg	gtg Val	ttt Phe	gtg Val 488	aaa Lys	aac Asn	agt Ser	aac Asn	aat Asn 493	1668
gcc Ala 494	ctg Leu	gca Ala	tgg Trp	gag Glu	aag Lys 499	acc Thr	acg Thr	agt Ser	gag Glu	gat Asp 504	gaa Glu	aag Lys	tgg Trp	aag Lys	aca Thr 509	1716
ggg Gly 510	aaa Lys	att Ile	cag Gln	ttg Leu	tat Tyr 515	caa Gln	gga Gly	act Thr	gat Asp	gct Ala 520	acc Thr	aaa Lys	agc Ser	atc Ile	att Ile 525	1764
ttt Phe 526	gaa Glu	gca Ala	gaa Glu	cgt Arg	ggc Gly 531	aag Lys	ggc Gly	aaa Lys	acc Thr	ggc Gly 536	gaa Glu	atc Ile	gca Ala	gtg Val	gat Asp 541	1812



Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	Gly	Lys	Val	Ile	Cys	Pro	180	185	190
Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	195	200	205
His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	210	215	220
Asp	Ile	Asn	Glu	Cys	Thr	Met	Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	225	230	235
Asn	Cys	Phe	Asn	Thr	Gln	Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	245	250	255
Tyr	Lys	Gly	Asn	Gly	Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	260	265	270
Lys	Glu	Val	Leu	Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	275	280	285
Leu	Leu	Ala	His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	290	295	300
Val	Thr	Pro	Glu	Pro	Thr	Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	305	310	315
Pro	Phe	Asn	Tyr	Glu	Glu	Ile	Val	Ser	Arg	Gly	Gly	Asn	Ser	His	Gly	325	330	335
Gly	Lys	Lys	Gly	Asn	Glu	Glu	Lys	Met	Lys	Glu	Gly	Leu	Glu	Asp	Glu	340	345	350
Lys	Arg	Glu	Glu	Lys	Ala	Leu	Lys	Asn	Asp	Ile	Glu	Glu	Arg	Ser	Leu	355	360	365
Arg	Gly	Asp	Val	Phe	Phe	Pro	Lys	Val	Asn	Glu	Ala	Gly	Glu	Phe	Gly	370	375	380
Leu	Ile	Leu	Val	Gln	Arg	Lys	Ala	Leu	Thr	Ser	Lys	Leu	Glu	His	Lys	385	390	395
Asp	Leu	Asn	Ile	Ser	Val	Asp	Cys	Ser	Phe	Asn	His	Gly	Ile	Cys	Asp	405	410	415
Trp	Lys	Gln	Asp	Arg	Glu	Asp	Asp	Phe	Asp	Trp	Asn	Pro	Ala	Asp	Arg	420	425	430
Asp	Asn	Ala	Ile	Gly	Phe	Tyr	Met	Ala	Val	Pro	Ala	Leu	Ala	Gly	His	435	440	445
Lys	Lys	Asp	Ile	Gly	Arg	Leu	Lys	Leu	Leu	Leu	Pro	Asp	Leu	Gln	Pro	450	455	460
Gln	Ser	Asn	Phe	Cys	Leu	Leu	Phe	Asp	Tyr	Arg	Leu	Ala	Gly	Asp	Lys	465	470	475
Val	Gly	Lys	Leu	Arg	Val	Phe	Val	Lys	Asn	Ser	Asn	Asn	Ala	Leu	Ala	485	490	495
Trp	Glu	Lys	Thr	Thr	Ser	Glu	Asp	Glu	Lys	Trp	Lys	Thr	Gly	Lys	Ile	500	505	510

09607860 101300

Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala  
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 Glu Arg Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp Gly Val Leu  
 530 535 540  
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 ctgctacggg gtccgggccg ggcgcctccc gaggggggct caggaggagg aaggaggacc 180  
 cgtgcgaga atg cct ctg ccc tgg agc ctt gcg ctc ccg ctg ctg ctc 228  
 Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Leu  
 1 5 10  
 tcc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt gca agg cat cat 276  
 Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg His His  
 14 19 24 29  
 cac ggg ttg tta gca tgc gca cgt cag cct ggg gtc tgt cac tat gga 324  
 His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly  
 30 35 40 45  
 act aaa ctg gcc tgc tgc tac ggc tgg aga aga aac agc aag gga gtc 372  
 Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val  
 46 51 56 61  
 tgt gaa gct aca tgc gaa cct gga tgt aag ttt ggt gag tgc gtg gga 420  
 Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly  
 62 67 72 77  
 cca aac aaa tgc aga tgc ttt cca gga tac acc ggg aaa acc tgc agt 468  
 Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser  
 78 83 88 93  
 caa gat gtg aat gag tgt gga atg aaa ccc cgg cca tgc caa cac aga 516  
 Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg  
 94 99 104 109  
 tgt gtg aat aca cac gga agc tac aag tgc ttt tgc ctc agt ggc cac 564  
 Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His  
 110 115 120 125

0968750 101300



atg ctc atg cca gat gct acg tgt gtg aac tct agg aca tgt gcc atg	612
Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala Met	
126 131 136 141	
ata aac tgt cag tac agc tgt gaa gac aca gaa gaa ggg cca cag tgc	660
Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln Cys	
142 147 152 157	
ctg tgt cca tcc tca gga ctc cgc ctg gcc cca aat gga aga gac tgt	708
Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp Cys	
158 163 168 173	
cta gat att gat gaa tgt gcc tct ggt aaa gtc atc tgt ccc tac aat	756
Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr Asn	
174 179 184 189	
cga aga tgt gtg aac aca ttt gga agc tac tac tgc aaa tgt cac att	804
Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile	
190 195 200 205	
ggg ttc gaa ctg caa tat atc agt gga cga tat gac tgt ata gat ata	852
Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile	
206 211 216 221	
aat gaa tgt act atg gat agc cat acg tgc agc cac cat gcc aat tgc	900
Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His Ala Asn Cys	
222 227 232 237	
ttc aat acc caa ggg tcc ttc aag tgt aaa tgc aag cag gga tat aaa	948
Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Lys	
238 243 248 253	
ggc aat gga ctt cgg tgt tct gct atc cct gaa aat tct gtg aag gaa	996
Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu	
254 259 264 269	
gtc ctc aga gca cct ggt acc atc aaa gac aga atc aag aag ttg ctt	1044
Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu	
270 275 280 285	
gct cac aaa aac agt atg aaa aag aag gca aaa att aaa aat gtt acc	1092
Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val Thr	
286 291 296 301	
cca gaa ccc acc agg act cct acc cct aag gtg aac ttg cag ccc ttc	1140
Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro Phe	
302 307 312 317	
aac tat gaa gag ata gtt tcc aga ggc ggg aac tct cat gga ggt aaa	1188
Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly Lys	
318 323 328 333	
aaa ggg aat gaa gag aaa atg aaa gag ggg ctt gag gat gag aaa aga	1236
Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys Arg	
334 339 344 349	
gaa gag aaa gcc ctg aag aat gac ata gag gag cga agc ctg cga gga	1284
Glu Glu Lys Ala Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg Gly	
350 355 360 365	
gat gtg ttt ttc cct aag gtg aat gaa gca ggt gaa ttc ggc ctg att	1332
Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu Ile	
366 371 376 381	

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ctg gtc caa agg aaa gcg cta act tcc aaa ctg gaa cat aaa gat tta	1380
Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His Lys Asp Leu	
382 387 392 397	
aat atc tcg gtt gac tgc agc ttc aat cat ggg atc tgt gac tgg aaa	1428
Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys Asp Trp Lys	
398 403 408 413	
cag gat aga gaa gat gat ttt gac tgg aat cct gct gat cga gat aat	1476
Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg Asp Asn	
414 419 424 429	
gct att ggc ttc tat atg gca gtt ccg gcc ttg gca ggt cac aag aaa	1524
Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys	
430 435 440 445	
gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa ccc caa agc	1572
Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro Gln Ser	
446 451 456 461	
aac ttc tgt ttg ctc ttt gat tac cgg ctg gcc gga gac aaa gtc ggg	1620
Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys Val Gly	
462 467 472 477	
aaa ctt cga gtg ttt gtg aaa aac agt aac aat gcc ctg gca tgg gag	1668
Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu	
478 483 488 493	
aag acc acg agt gag gat gaa aag tgg aag aca ggg aaa att cag ttg	1716
Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile Gln Leu	
494 499 504 509	
tat caa gga act gat gct acc aaa agc atc att ttt gaa gca gaa cgt	1764
Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg	
510 515 520 525	
ggc aag ggc aaa acc ggc gaa atc gca gtg gat ggc gtc ttg ctt gtt	1812
Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp Gly Val Leu Leu Val	
526 531 536 541	
tca ggc tta tgt cca gat agc ctt tta tct gtg gat gac tga atgttac	1861
Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val Asp Asp *	
542 547 552	
tatctttata tttgactttg tatgtcagtt ccctggtttt tttgatattg catcatagga	1921
cctctggcat tttagaatta ctagctgaaa aattgtaatg taccaacaga aatattattg	1981
taagatgcct ttcttgata agatatgcca atatttgctt taaatatcat atcactgtat	2041
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aaaa	2345

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 <212> PRT  
 <213> Homo sapiens

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Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	Ala	Arg	His	His	His	Gly	Leu
			20					25					30		
Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	Lys	Leu
		35					40					45			
Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	Cys	Glu	Ala
	50					55					60				
Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	Gly	Pro	Asn	Lys
65					70					75					80
Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser	Gln	Asp	Val
				85					90					95	
Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg	Cys	Val	Asn
			100					105					110		
Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met
		115					120					125			
Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys
	130					135					140				
Gln	Tyr	Ser	Cys	Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro
145					150					155					160
Ser	Ser	Gly	Leu	Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile
				165					170					175	
Asp	Glu	Cys	Ala	Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys
			180					185					190		
Val	Asn	Thr	Phe	Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu
		195					200					205			
Leu	Gln	Tyr	Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys
	210					215					220				
Thr	Met	Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr
225					230					235					240
Gln	Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly
				245					250					255	
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	Arg
			260					265					270		
Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	His	Lys
		275					280						285		

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Asn Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro  
 290 295 300

Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu  
 305 310 315 320

Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn  
 325 330 335

Glu Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys  
 340 345 350

Ala Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe  
 355 360 365

Phe Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln  
 370 375 380

Arg Lys Ala Leu Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser  
 385 390 395 400

Val Asp Cys Ser Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg  
 405 410 415

Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly  
 420 425 430

Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys Asp Ile Gly  
 435 440 445

Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys  
 450 455 460

Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg  
 465 470 475 480

Val Phe Val Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr  
 485 490 495

Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly  
 500 505 510

Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly  
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Cys Pro Asp Ser Leu Leu Ser Val Asp Asp  
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ggaggaccgc	tgcgaga	atg	cct	ctg	ccc	tgg	agc	ctt	gcg	ctc	ccg	ctg		290		
		Met	Pro	Leu	Pro	Trp	Ser	Leu	Ala	Leu	Pro	Leu				
		1					5				10					
ctg	ctc	tcc	tgg	gtg	gca	ggg	ggg	ttc	ggg	aac	gcg	gcc	agt	gca	agg	338
Leu	Leu	Ser	Trp	Val	Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	Ala	Arg	
			15					20					25			
cat	cac	ggg	ttg	tta	gca	tgc	gca	cgt	cag	cct	ggg	gtc	tgt	cac	tat	386
His	His	Gly	Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	
		30					35					40				
gga	act	aaa	ctg	gcc	tgc	tgc	tac	ggc	tgg	aga	aga	aac	agc	aag	gga	434
Gly	Thr	Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	
	45					50					55					
gtc	tgt	gaa	gct	aca	tgc	gaa	cct	gga	tgt	aag	ttt	ggg	gag	tgc	gtg	482
Val	Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	
	60				65					70					75	
gga	cca	aac	aaa	tgc	aga	tgc	ttt	cca	gga	tac	acc	ggg	aaa	acc	tgc	530
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	
				80					85					90		
agt	caa	gat	gtg	aat	gag	tgt	gga	atg	aaa	ccc	cgg	cca	tgc	caa	cac	578
Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	Gln	His	
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aga	tgt	gtg	aat	aca	cac	gga	agc	tac	aag	tgc	ttt	tgc	ctc	agt	ggc	626
Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	
			110				115					120				
cac	atg	ctc	atg	cca	gat	gct	acg	tgt	gtg	aac	tct	agg	aca	tgt	gcc	674
His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	Arg	Thr	Cys	Ala	
	125					130					135					
atg	ata	aac	tgt	cag	tac	agc	tgt	gaa	gac	aca	gaa	gaa	ggg	cca	cag	722
Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	
	140				145					150					155	
tgc	ctg	tgt	cca	tcc	tca	gga	ctc	cgc	ctg	gcc	cca	aat	gga	aga	gac	770
Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	
				160					165					170		
tgt	cta	gat	att	gat	gaa	tgt	gcc	tct	ggg	aaa	gtc	atc	tgt	ccc	tac	818
Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	
			175					180					185			
aat	cga	aga	tgt	gtg	aac	aca	ttt	gga	agc	tac	tac	tgc	aaa	tgt	cac	866
Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	
		190					195									

ata	aat	gaa	tgt	act	atg	gat	agc	cat	acg	tgc	agc	cac	cat	gcc	aat	962
Ile	Asn	Glu	Cys	Thr	Met	Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	
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tgc	ttc	aat	acc	caa	ggg	tcc	ttc	aag	tgt	aaa	tgc	aag	cag	gga	tat	1010
Cys	Phe	Asn	Thr	Gln	Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	
				240					245					250		
aaa	ggc	aat	gga	ctt	cgg	tgt	tct	gct	atc	cct	gaa	aat	tct	gtg	aag	1058
Lys	Gly	Asn	Gly	Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	
			255					260					265			
gaa	gtc	ctc	aga	gca	cct	ggg	acc	atc	aaa	gac	aga	atc	aag	aag	ttg	1106
Glu	Val		Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	
		270					275					280				
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Leu	Ala	His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	
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Gly	Asp	Val	Phe	Phe	Pro	Lys	Val	Asn	Glu	Ala	Gly	Glu	Phe	Gly	Leu	
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Asp	Leu	Asn	Ile	Ser	Val	Asp	Cys	Ser	Phe	Asn	His	Gly	Ile	Cys	Asp	
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tgg	aaa	cag	gat	aga	gaa	gat	gat	ttt	gac	tgg	aat	cct	gct	gat	cga	1538
Trp	Lys	Gln	Asp	Arg	Glu	Asp	Asp	Phe	Asp	Trp	Asn	Pro	Ala	Asp	Arg	
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Asp	Asn	Ala	Ile	Gly	Phe	Tyr	Met	Ala	Val	Pro	Ala	Leu	Ala	Gly	His	
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Lys	Lys	Asp	Ile	Gly	Arg	Leu	Lys	Leu	Leu	Leu	Pro	Asp	Leu	Gln	Pro	
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caa	agc	aac	ttc	tgt	ttg	ctc	ttt	gat	tac	cgg	ctg	gcc	gga	gac	aaa	1682
Gln	Ser	Asn	Phe	Cys	Leu	Leu	Phe	Asp	Tyr	Arg	Leu	Ala	Gly	Asp	Lys	
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			20					25					30		
Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	Lys	Leu	Ala
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Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	Cys	Glu	Ala	Thr
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Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser	Gln	Asp	Val	Asn
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Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys Asp Ile Gly  
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Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys  
450 455 460

Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg  
465 470 475 480

Val Phe Val Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr  
485 490 495

Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly  
500 505 510

Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly  
515 520 525

Lys Thr Gly Glu Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu  
530 535 540

Cys Pro Asp Ser Leu Leu Ser Val Asp Asp  
545 550

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